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RAW SEQUENCE LISTING

DATE: 10/24/2001

PATENT APPLICATION: US/09/970,076

TIME: 14:17:42

Input Set : A:\Uw977451.app

Output Set: N:\CRF3\10242001\I970076.raw

ENTERED

3 <110> APPLICANT: Young, John A.T.
4 Bradley, Kenneth A.
5 Collier, Robert J.
6 Mogridge, Jeremy S.
8 <120> TITLE OF INVENTION: Anthrax Toxin Receptor
10 <130> FILE REFERENCE: 960296.97745
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/970,076 *OK*
C--> 13 <141> CURRENT FILING DATE: 2001-10-03
15 <150> PRIOR APPLICATION NUMBER: 60/251,481
16 <151> PRIOR FILING DATE: 2000-12-05
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 1414
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (104)..(1207)
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34 agcgtgggaa ggagcggacc ctgctctccc cgggctgcgg gcc atg gcc acg gcg 115
35 Met Ala Thr Ala
36 1
38 gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act 163
39 Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr
40 5 10 15 20
42 ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt 211
43 Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly
44 25 30 35
46 cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259
47 Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
48 40 45 50
50 gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307
51 Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
52 55 60 65
54 ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt 355
55 Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
56 70 75 80
58 ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac aga gaa 403
59 Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu
60 85 90 95 100
62 caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca gga gga 451
63 Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly
64 105 110 115
66 gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag att tat 499
67 Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr

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68          120          125          130
70 tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att gct ttg 547
71 Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu
72          135          140          145
74 act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag agg gag 595
75 Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu
76          150          155          160
78 gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt ggt gtg 643
79 Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val
80 165          170          175          180
82 aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt aag gat 691
83 Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp
84          185          190          195
86 cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc atc atc 739
87 His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile
88          200          205          210
90 cac tca att ttg aag aag tcc tgc atc gaa att cta gcag gct gaa cca 787
91 His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro
92          215          220          225
94 tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga gga aac 835
95 Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn
96          230          235          240
98 ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc ttc aag 883
99 Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys
100 245          250          255          260
102 atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg gaa gac 931
103 Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val Glu Asp
104          265          270          275
106 act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc atg aaa 979
107 Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys
108          280          285          290
110 gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc tcc agt 1027
111 Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser
112          295          300          305
114 tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc 1075
115 Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala
116          310          315          320
118 atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg 1123
119 Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp
120 325          330          335          340
122 tgg ttc tgg ccc ctc tgc tgc act gtg att atc aag gag gtc cct cca 1171
123 Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro
124          345          350          355
126 ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag 1217
127 Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
128          360          365
130 aagaaagaaa gaaatccac agaaacagat aacctaacac agcccgtaga acgtatttta 1277
132 tacaatgctc tgaaaatcat agtctcaatc tagacagtct tttcctctag ttccctgtat 1337
134 tcaaatccca gtgtctaaca ttcaataaat agctatatga aatcaaaaaa aaaaaaaaaa 1397

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1414

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136 aaaaaaaaaa aaaaaaa
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 368
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
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146   1           5           10           15
148 Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
149           20           25           30
151 Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
152           35           40           45
154 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
155           50           55           60
157 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
158   65           70           75           80
160 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
161           85           90           95
163 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
164           100          105          110
166 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
167           115          120          125
169 Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
170           130          135          140
172 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
173 145           150          155          160
175 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
176           165          170          175
178 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
179           180          185          190
181 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
182           195          200          205
184 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
185           210          215          220
187 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
188 225           230          235          240
190 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
191           245          250          255
193 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
194           260          265          270
196 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
197           275          280          285
199 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
200           290          295          300
202 Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
203 305           310          315          320
205 Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
206           325          330          335
208 Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys

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209          340          345          350
211 Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
212          355          360          365
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 180
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: von Willebrand
223      factor A domain consensus sequence
225 <400> SEQUENCE: 3
226 Pro Leu Asp Val Val Phe Leu Leu Asp Gly Ser Gly Ser Met Gly Gly
227   1          5          10          15
229 Asn Arg Phe Glu Leu Ala Lys Glu Phe Val Leu Lys Leu Val Glu Gln
230          20          25          30
232 Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser
233          35          40          45
235 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
236          50          55          60
238 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
239  65          70          75          80
241 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
242          85          90          95
244 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
245          100         105         110
247 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
248          115         120         125
250 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
251          130         135         140
253 Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
254 145         150         155         160
256 Gly Val Phe Ala Val Glu Asp Leu Pro Glu Leu Leu Asp Leu Leu Ile
257          165         170         175
259 Asp Leu Leu Leu
260          180
263 <210> SEQ ID NO: 4
264 <211> LENGTH: 198
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 4
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272 Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu Glu Lys Phe Val Gln
273          20          25          30
275 Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val Gly Leu Ile Gln Tyr
276          35          40          45
278 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
279          50          55          60
281 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp

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282 65          70          75          80
284 Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
285          85          90          95
287 Ser Ala Ser Gly Gly Arg Arg Ser Ala Ala Thr Lys Val Met Val Val
288          100          105          110
290 Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
291          115          120          125
293 Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
294          130          135          140
296 Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
297 145          150          155          160
299 Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
300          165          170          175
302 Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly Thr Leu Gly Glu Gln
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305 Ile Phe Ser Ile Glu Gly
306          195
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310 <211> LENGTH: 5540
311 <212> TYPE: DNA
312 <213> ORGANISM: Homo sapiens
314 <220> FEATURE:
315 <221> NAME/KEY: CDS
316 <222> LOCATION: (144)..(1835)
318 <400> SEQUENCE: 5
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321 cgcgatggc gcgccctga gggctgtggc gagttcgcg agcgtgggaa ggagcggacc 120
323 ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gcc ctc gcc 173
324          Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
325          1          5          10
327 atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
328 Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
329          15          20          25
331 ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
332 Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
333          30          35          40
335 ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac 317
336 Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
337          45          50          55
339 tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc 365
340 Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile
341          60          65          70
343 agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca 413
344 Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
345 75          80          85          90
347 acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 461
348 Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
349          95          100          105
351 gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 509

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/970,076

DATE: 10/24/2001

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date